STIC Biotechnology Systems Branch
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10 532,681
Source: PCT
Date Processed by STIC: 1-23-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/532,681

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ___ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or **Xaa**, and which residue n or **Xaa** represents.

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa

"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

```
   3 <110> APPLICANT: LUKYANOV, Sergei Anatolievich
   4         SHAGIN, Dmitry Alexeevich
   5         YANUSHEVICH, Yury Grigorievich
   7 <120> TITLE OF INVENTION: FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-
AEQUOREA HYDROZOA
   8         SPECIES AND METHODS FOR USING SAME
  10 <130> FILE REFERENCE: U 015745-9
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/532,681
  11 <141> CURRENT FILING DATE: 2005-04-26
  13 <160> NUMBER OF SEQ ID NOS: 22
  15 <170> SOFTWARE: PatentIn version 3.1
```

Does Not Comply
Corrected Diskette Needed
(Pg.1-5)

ERRORED SEQUENCES

```
  134 <210> SEQ ID NO: 5
  135 <211> LENGTH: 705
  136 <212> TYPE: DNA
  137 <213> ORGANISM: Artificial sequence
W--> 138 <220> FEATURE:
  139 <223> OTHER INFORMATION: phiYFP-M0 mutant of the phiYFP
W--> 140 <400> SEQUENCE: 5
  142 atgcctagtg gagcactgtt gttccacgga aagatcccat atgttgttga gatggaggga      60
  143 aatgttgatg gacacacatt ctccattaga ggtaaaggtt atggagatgc aagtgttggt     120
  144 aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta     180
  145 gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat     240
E--> 146
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg     300gacggaaact t
  147 gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa     420
  148 ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag     480
  149 tctgctttca aaattcgcca tgagattact ggataaaag gagacttcat tgttgcagac     540
  150 cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat     600
  151 atgagctacc atgtcaagct cagcaaagat gttactgatc acaggataaa catgagcttg     660
  152 aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa     705
  275 <210> SEQ ID NO: 10
  276 <211> LENGTH: 234
  277 <212> TYPE: PRT
  278 <213> ORGANISM: Artificial sequence
W--> 279 <220> FEATURE:
  280 <223> OTHER INFORMATION: humanized version of the phiYFP-M1
W--> 281 <400> SEQUENCE: 10
  283 Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
  284 1               5                  10                  15
  285 Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
```

See item # 1 on error Summary Sheet.

286   20   25   30

Input Set : A:\u0157459 sequence listing.txt
Output Set: N:\CRF4\01232006\J532681.raw

```
287 Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
288         35                  40                  45
289 Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
290         50                  55                  60
292 Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
293 65                  70                  75                  80
294 Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
295                 85                  90                  95
296 Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
297                 100                 105                 110
298 Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
299         115                 120                 125
300
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr        130
    301 Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
E--> 302 145                 150                 155                 160
    303 Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
E--> 304   .       -           165                 170                 175
    305 Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
E--> 306                 180                 185                 190
    307 Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
E--> 308         195                 200                 205
    309 Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
E--> 310         210                 215                 220
    311 Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
E--> 312 225                 230
    406 <210> SEQ ID NO: 14
    407 <211> LENGTH: 232
    408 <212> TYPE: PRT
    409 <213> ORGANISM: hydromedusa 2 from sub-order Anthomedusae
W--> 410 <400> SEQUENCE: 14
    412 Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
    413 1               5                  10                  15
    414 Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
    415                 20                  25                  30
    416 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
    417         35                  40                  45
    418 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    419         50                  55                  60
    420 Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
    421 65                  70                  75                  80
    422 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
    423                 85                  90                  95
    424 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
    425                 100                 105                 110
    426 Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
    427         115                 120                 125
    428 Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
    429         130                 135                 140
    430 Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
```

See item #1 on error summary sheet.

Insert on line 12207-12237

RAW SEQUENCE LISTING   DATE: 01/23/2006
PATENT APPLICATION: US/10/532,681   TIME: 09:12:04

Input Set : A:\u0157459 sequence listing.txt
Output Set: N:\CRF4\01232006\J532681.raw

[handwritten: —See item #1 on error Summary Sheet]

```
E--> 431
145               150               155               160 Cys Tyr Ile Gly Phe
E--> 432                165               170               175
    433 Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
E--> 434          180               185               190
    435 Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
E--> 436          195               200               205
    437 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
E--> 438     210               215               220
    439 Val Pro Arg Ile Thr Ser Ala Ile
E--> 440 225               230
    442 <210> SEQ ID NO: 15
    443 <211> LENGTH: 699
    444 <212> TYPE: DNA
    445 <213> ORGANISM: Artificial sequence
W--> 446 <220> FEATURE:
    447 <223> OTHER INFORMATION: S3-2 mutant of the hm2CP
W--> 448 <400> SEQUENCE: 15
    450 atggaaggtg gtccagcatt atttcaatcc gacatgacat tcaagatctt catcgatgga      60
    451 gtggtgaatg gtcagaaatt cacgatagtc gcagatggat cgtccaaatt cccccatggt     120
    452 gacttcaacg tacatgctgt gtgcgaaacc gggaaactcc caatgtcatg gaaacccatt     180
    453 tgtcacctta tccaatacgg ggagccattc tttgcaagat atcccaacgg catcagccat     240
    454 tttgcacagg agtgctttcc agaaggatta tcaattgatc gaacagtcag attcgaaaat     300
    455 gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg     360
E--> 456
ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttgtt     420gatatcctgc
    457 gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa     540
    458 atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata     600
    459 accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc     660
    460 tacgctcact cagttccacg catcacttct gctatctaa                            699
    563 <210> SEQ ID NO: 19
    564 <211> LENGTH: 705
    565 <212> TYPE: DNA
    566 <213> ORGANISM: Artificial sequence
W--> 567 <220> FEATURE:
    568 <223> OTHER INFORMATION: phiYFP-M1C1 mutant, derived from humanized
version of the phiYFP-
    569       M1
W--> 570 <400> SEQUENCE: 19
    572 atgtccagcg gcgcccagct gttccacggc aagatccct acgtggtgga gatggagggc      60
    573 aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc     120
    574 aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg     180
    575 gtgaccaccc tgtcctgggg cgcccagtgc ttcgccaagt acggccccga gctgaaggat     240
    576 ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc     300
E--> 577
gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc     360gtgaagctga a
    578 ttcaatttca ccccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag     480
    579 agcgccttca gatctgcca cgagatcacc ggcagtaagg gcgatttcat cgtggccgat     540
    580 cacacccaga tgaataccccc atcggcggc ggccccgtgc acgtgcccga gtaccaccac     600
    581 atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg     660
    582 aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga                     705
    645 <210> SEQ ID NO: 22
    646 <211> LENGTH: 232
```

[handwritten annotations: —See item #11 on error summary sheet; What is the source of genetic material? ; Same error ; Same error]

```
       647 <212> TYPE: PRT
       648 <213> ORGANISM: Artificial sequence
W-->   649 <220> FEATURE:
       650 <223> OTHER INFORMATION: humanized S3-2 mutant
W-->   651 <400> SEQUENCE: 22
       653 Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
       654 1               5                   10                  15
       656 Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
       657             20                  25                  30
       658 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
       659         35                  40                  45
       660 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
       661     50                  55                  60
       662 Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
       663 65                  70                  75                  80
       664 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
       665                 85                  90                  95
       666 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
       667             100                 105                 110
       668 Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
       669         115                 120                 125
       670 Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
       671     130                 135                 140
       672 Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
       673 145                 150                 155                 160
       674 Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
       675                 165                 170                 175
       676 Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
       677             180                 185                 190
       678 Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
       679         195                 200                 205
       680 Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
       681     210                 215                 220
       682 Val Pro Arg Ile Thr Ser Ala Ile
       683 225                 230
E-->   687 1
```

[handwritten annotation: circled "1" with "pls delete"]

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/23/2006
PATENT APPLICATION: **US/10/532,681**   TIME: 09:12:05

Input Set : **A:\u0157459 sequence listing.txt**
Output Set: **N:\CRF4\01232006\J532681.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 146
Seq#:10; Line(s) 300
Seq#:14; Line(s) 431
Seq#:15; Line(s) 456
Seq#:19; Line(s) 577

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/532,681**

DATE: 01/23/2006
TIME: 09:12:05

Input Set : **A:\u0157459 sequence listing.txt**
Output Set: **N:\CRF4\01232006\J532681.raw**

L:11 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION
NUMBER: is Added.
L:16 M:283 W: Missing Blank Line separator, <210> field identifier
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:138 M:283 W: Missing Blank Line separator, <220> field identifier
L:140 M:283 W: Missing Blank Line separator, <400> field identifier
L:146 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:158 M:283 W: Missing Blank Line separator, <220> field identifier
L:160 M:283 W: Missing Blank Line separator, <400> field identifier
L:198 M:283 W: Missing Blank Line separator, <220> field identifier
L:200 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:221 M:283 W: Missing Blank Line separator, <400> field identifier
L:258 M:283 W: Missing Blank Line separator, <220> field identifier
L:260 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:283 W: Missing Blank Line separator, <220> field identifier
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:302 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:304 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:306 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:308 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:310 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:312 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:312 M:252 E: No. of Seq. differs, <211> LENGTH:Input:234 Found:218 SEQ:10
L:318 M:283 W: Missing Blank Line separator, <400> field identifier
L:343 M:283 W: Missing Blank Line separator, <400> field identifier
L:384 M:283 W: Missing Blank Line separator, <400> field identifier
L:410 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:432 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:434 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:436 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:438 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:440 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:446 M:283 W: Missing Blank Line separator, <220> field identifier
L:448 M:283 W: Missing Blank Line separator, <400> field identifier
L:456 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:466 M:283 W: Missing Blank Line separator, <220> field identifier
L:468 M:283 W: Missing Blank Line separator, <400> field identifier
L:505 M:283 W: Missing Blank Line separator, <220> field identifier
L:508 M:283 W: Missing Blank Line separator, <400> field identifier
L:526 M:283 W: Missing Blank Line separator, <220> field identifier
L:529 M:283 W: Missing Blank Line separator, <400> field identifier
L:567 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY   DATE: 01/23/2006
PATENT APPLICATION: **US/10/532,681**   TIME: 09:12:05

Input Set : **A:\u0157459 sequence listing.txt**
Output Set: **N:\CRF4\01232006\J532681.raw**

L:570 M:283 W: Missing Blank Line separator, <400> field identifier
L:577 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:588 M:283 W: Missing Blank Line separator, <220> field identifier
L:591 M:283 W: Missing Blank Line separator, <400> field identifier
L:628 M:283 W: Missing Blank Line separator, <220> field identifier
L:630 M:283 W: Missing Blank Line separator, <400> field identifier
L:649 M:283 W: Missing Blank Line separator, <220> field identifier
L:651 M:283 W: Missing Blank Line separator, <400> field identifier
L:687 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22